

mammalian genome, but it can be found at close to its expected frequency in small genomic areas of about one kilobase, called CpG islands. Although the CpG islands account for only about 1% of the complete genome and for 15 % of the total genomic CpG sites, these regions contain approximately 50% of the unmethylated CpG dinucleotides. Methylation, may for example, impact disease states, such as Fragile X and Rett syndrome, and also on drug profiling. See for example, Robertson et al., *Nature Reviews*, 2000 vol 1, p. 11-19, and Esteller M. et al. *New England Journal of Medicine*, 2000, Vol 343:19, p. 1350-1354, the disclosures of which are hereby incorporated by reference.

In one embodiment, the at least one mutation that correlates to resistance to at least one therapy includes mutations or combinations of mutations that are known or suspected in the art to influence the sensitivity to a therapy. Lists of mutations known or suspected in the art to influence the sensitivity of a disease causing agent to a therapy may be found, for example, in the scientific literature, patents, and patent applications. For example, mutations known or suspected in the art to influence the sensitivity of HIV to a therapy may be found in, Schinazi, R.F., Larder, B.A. & Mellors, J.W. 1997. *Int. Antiretroviral News* 5, 129-142 (1997); Schinazi et al., *Intl. Antiretroviral News* 7, 46-69 (1999); Shafer et al., *Nucleic Acid Research*, 27(1), 348-352 (1999); WO 00/78996; WO 99/67427; WO 99/61658; US 6,087,093; WO 00/73511; and U.S. Patent Application Serial Nos. 09/580/491, 09/589,167^{now US Patent 7,058,616} and 60/241,844, the disclosures of which are hereby incorporated by reference. Examples of mutations known or suspected in the art to influence the sensitivity of HIV to a therapy may also be found on the